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Presence and expression of genes encoding hydrocarbon decomposition ability of microbes in different soil types sampled in tatarstan republic (Russia)

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Abstract

© SGEM 2018. Large areas of oil contaminated soil are an urgent problem in oil producing regions, such as the Republic of Tatarstan (Russia). One of important factors of soil self-restoration is the presence of members able to decompose hydrocarbons in the microbial community. Different groups of genes are responsible for decomposing different hydrocarbon groups: for example, alkane monooxygenase gene and naphthalene dioxygenase gene are the predominant genes corresponding to first-step hydroxylases involved in the metabolism of alkanes and aromatic hydrocarbons, respectively; genes encoding catechol 2,3-dioxygenase are capable of activating the decomposition of xylene, toluene and other PAHs. In this research, we investigated the presence and expression of genes encoding microbial ability to decompose hydrocarbons in pristine soils using qPCR and reverse transcription qPCR (RT-qPCR), respectively. We evaluated the distribution of the genes of alkane-monooxygenase (alkB, alkM and alkB), genes encoding dioxygenase xylE (Sphingobium-like catechol 2,3-dioxygenase), cat2,3 (catechol 2,3-dioxygenase, related to the genera Pseudomonas, Sphingomonas and Bacillus) and nah (naphthalene dioxygenase). The most abundant group was the alkB and alkB1 genes, associated with the representatives of the genera Pseudomonas (Ps. fluorescens, Ps. aeruginosa), Rhodococcus, Burkholderia and Amycolatopsis. These genes were present in all soil samples and ranged from 2.8×103 to 3.5×106 gene copies number g-1. The alkB genes belonging to the representatives of the species Pseudomonas putida and genus Stenotrophomonas were detected in 20 samples and ranged from 1.6×102 to 2.0×104 gene copies number g-1. The gene alkM, belonging to the genus Acinetobacter was not detected in any of the samples. Genes responsible for the encoding of dioxygenases were detected in only 10 soil samples in insignificant amounts: cat2,3 – in the range of 1.1×103 to 8.3×103 gene copies number g-1, xylE-2.0×102 to 4.9×103 gene copies number g-1. The nah gene responsible for the encoding of naphthalene-dioxygenase was detected in 13 samples in the range of 1.6×102 to 1.8×104 gene copies number g-1. The analysis of expression of hydrocarbon degrading genes under investigaion showed negative expression in all the samples. Thus, genes responsible for the degradation of hydrocarbons (alkB and alkB1, xylE, cat2,3) were detected in pristine soils in the Republic of Tatarstan, however, the expression of the identified genes did not occur. The alkM gene was not detected.

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Keywords

3-dioxygenase, Alkane monooxygenase, Catechol 2, Gene abundance, Gene expression, Naphthalene dioxygenase, Pristine soil

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